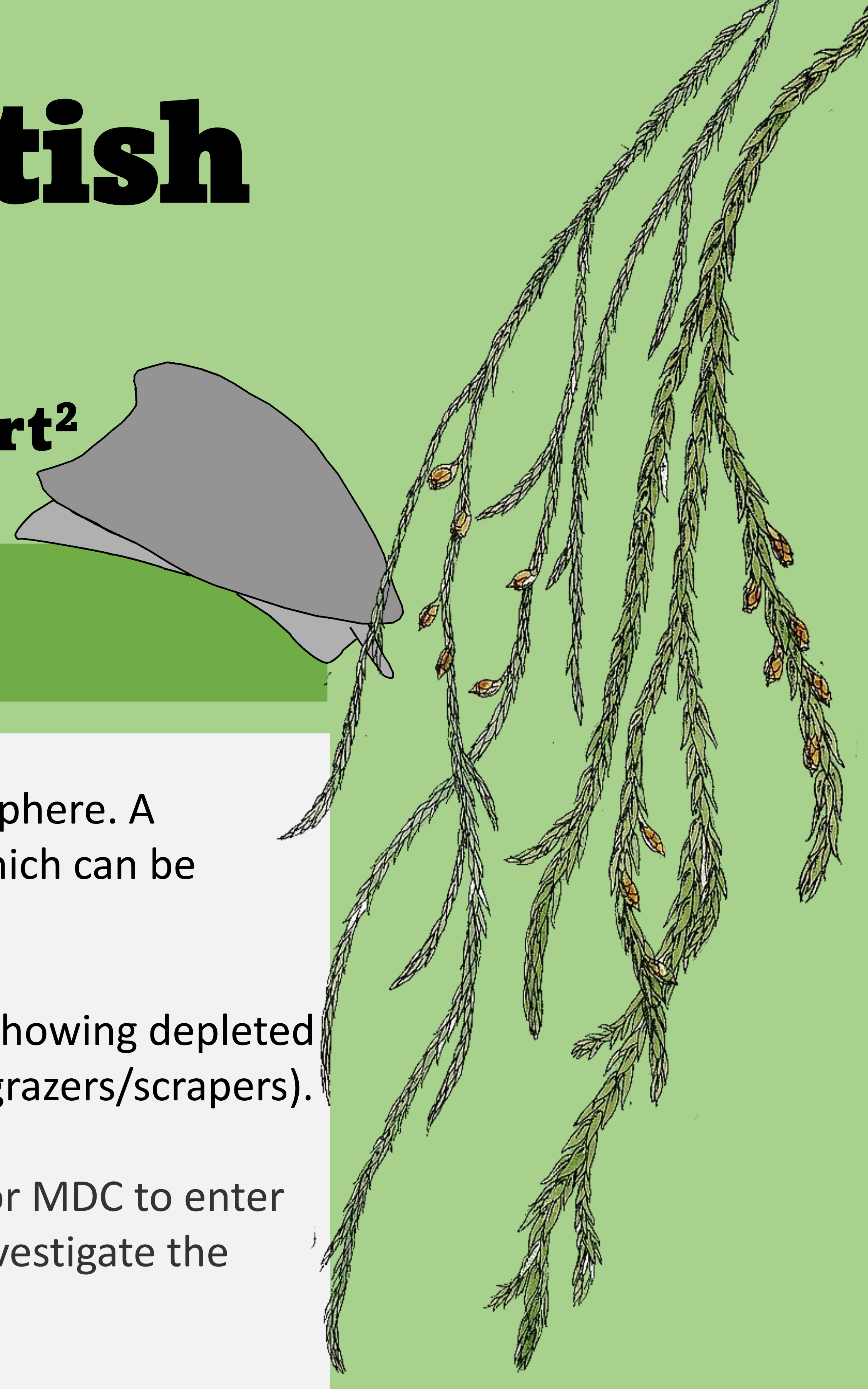
Is Methane Fuelling Scottish Streams?

Michael Hinchliffe[1], Rob Briers[1], Aimeric Blaud[1] & Peter Gilbert[2]

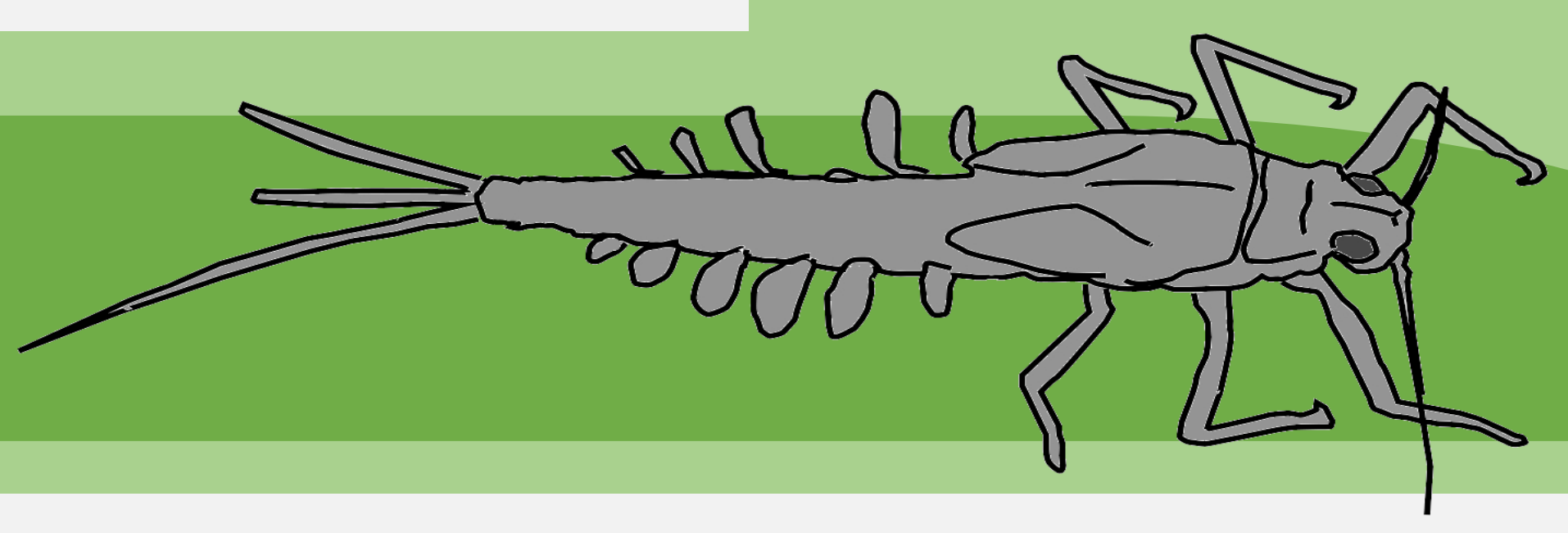


Introduction

Streams and rivers are frequently supersaturated with methane, but not all of this is emitted to the atmosphere. A significant proportion is oxidised by microorganisms and sequestered into biomass or converted to CO_2 which can be utilised by plants for photosynthesis.

Initial analysis of stream communities within the River Tweed catchment identified five invertebrate taxa showing depleted $\delta^{13}C$ values, indicative of methane derived carbon (MDC). All five taxa shared a functional feeding group (grazers/scrapers).

Here we investigate stable isotope values of the different taxa and basal resources to examine pathways for MDC to enter the food web, evaluate variation in the incorporation of MDC between areas of different flow rates and investigate the distribution and characteristics of the methane-related microbial community within streams.



Methods

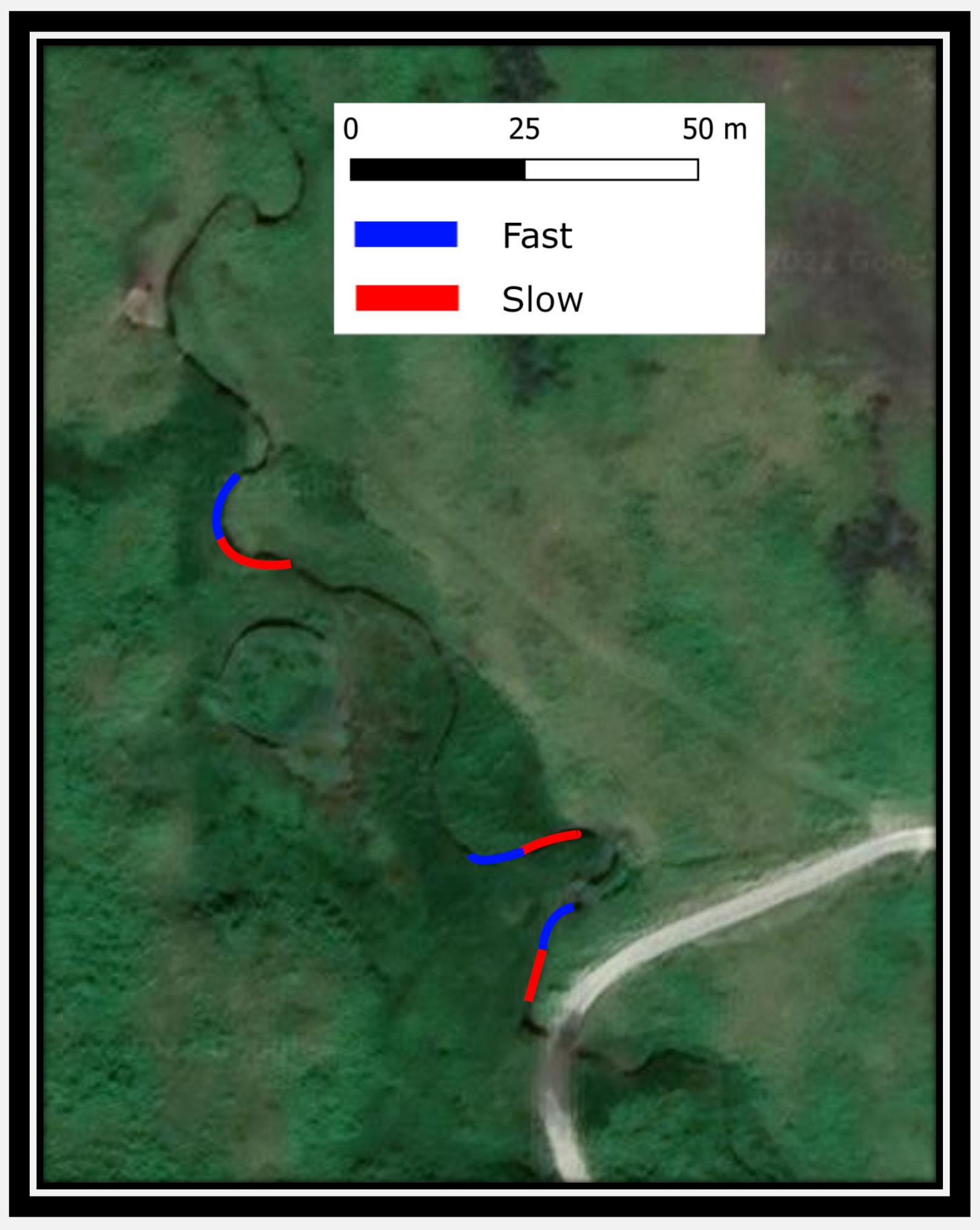


Figure 1 – Map of a sample stream with Fast and Slow sections marked

3 Streams in the Tweed catchment
3 slow flowing sections, 3 fast flowing sampled in each (see Fig 1). Sampling included:

- Dominant Macrophyte (*Callitriche sp*./crowfoot)
- Dominant Bryophyte (*Fontinalis antipyretica*)
- 5 grazing taxa (*Baetis sp.*, Heptageniidae, *A.fluviatilis*, Glossosomatidae, Goeridae)
- Rock biofilms (Fig 2)
- Terrestrial detritus
- Methane concentrations
- Environmental conditions (pH, temp etc)

All samples were analysed for their carbon and nitrogen stable isotope values

A combination of PCR, qPCR and sequencing techniques will be employed to identify presence and abundance of:

- Methane producing archaea (methanogens)
- Methane oxidising Bacteria (MOB):
  - Type I MOB
  - Type II MOB

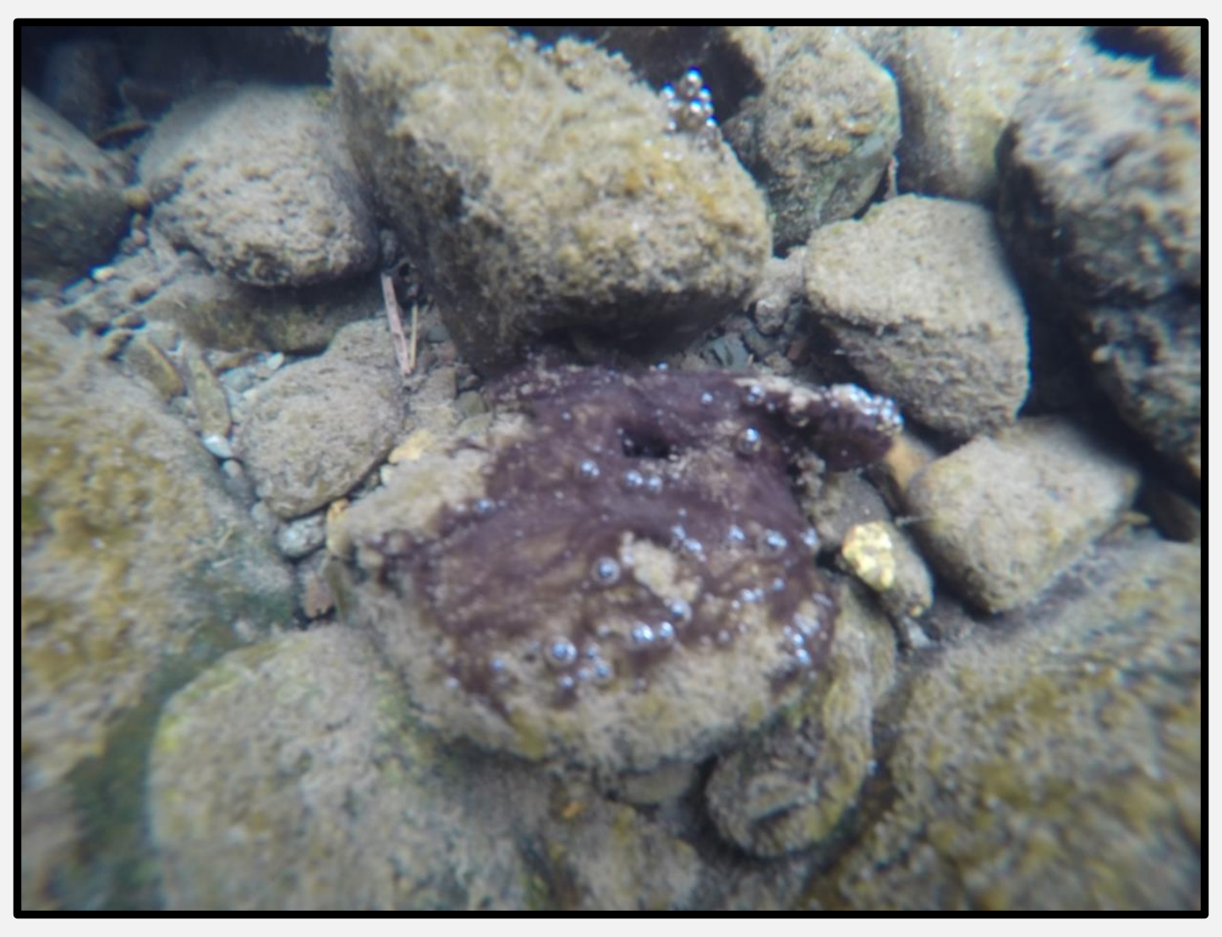
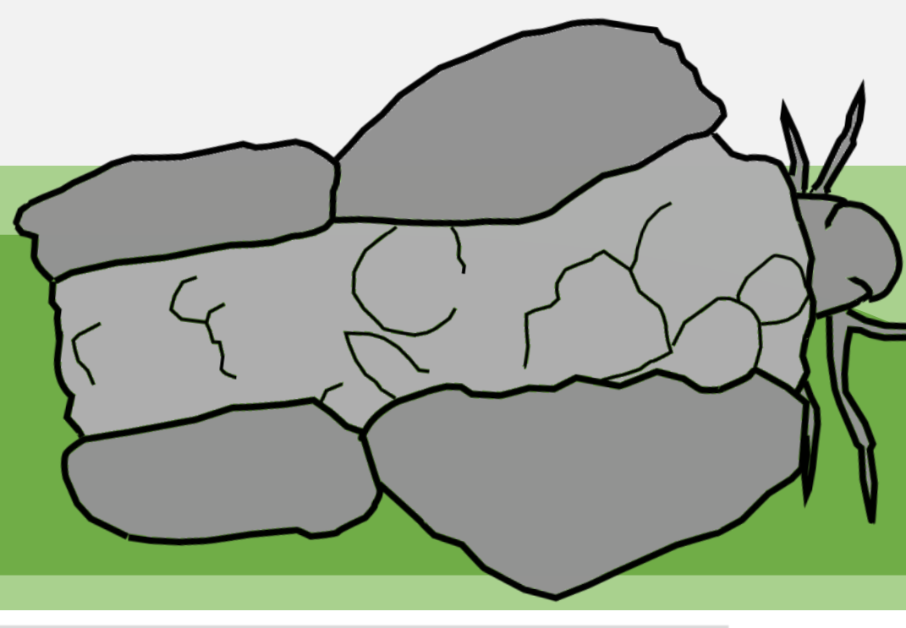


Figure 2 – Rock biofilms



Results So Far

Initial PCR results from *F.antipyretica* and *Callitriche sp.* (Figure 3) have confirmed the presence of methanogens and both type I and type II MOB.

MOB presence was found in all *F.antipyretica* samples and 2/3 of the *Callitriche sp. S*amples.

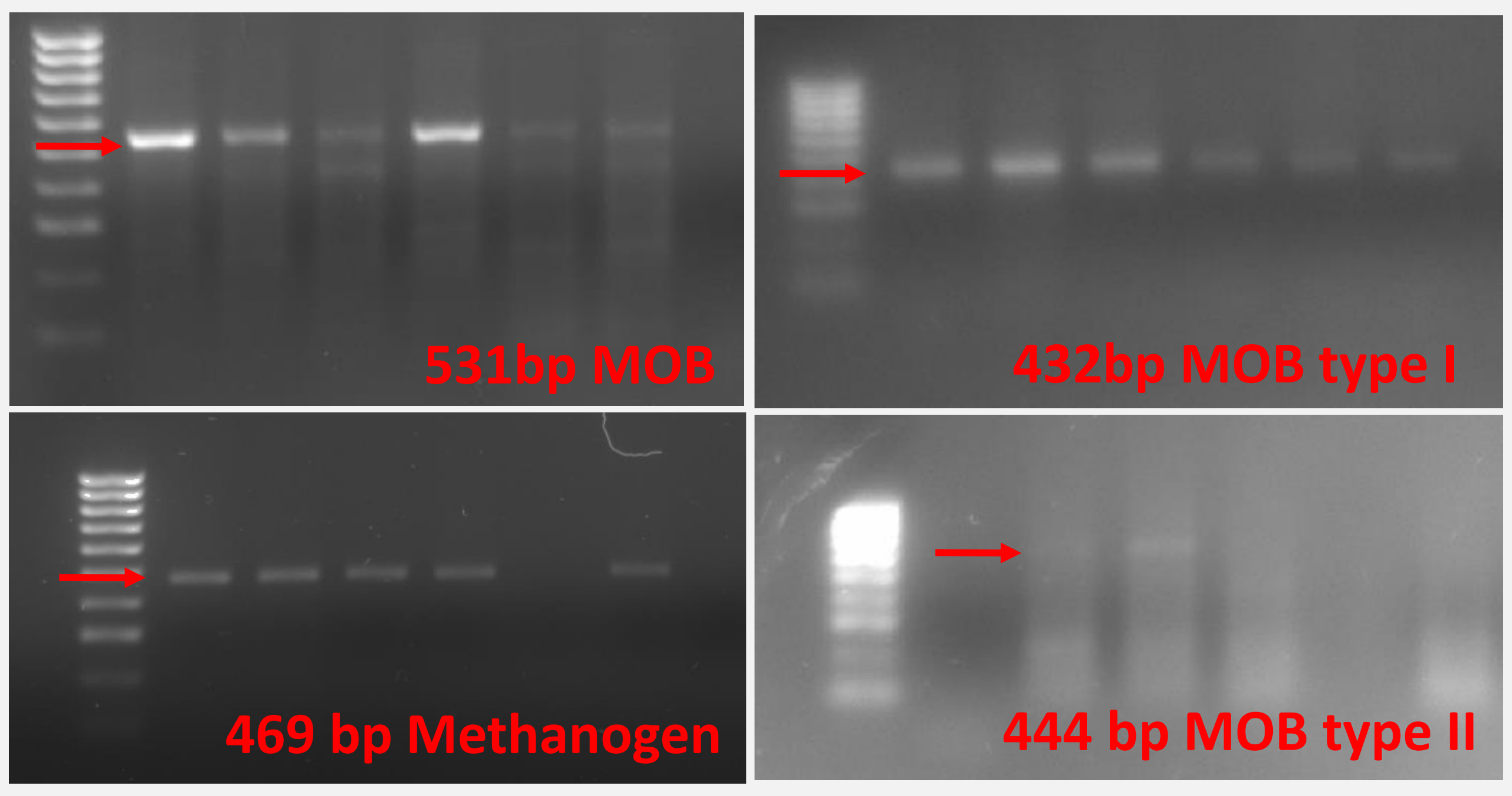


Figure 3 – PCR results for MOB (top left) methanogen (bottom left) MOB type I (top right) MOB type II (bottom right). Columns 1-3: *F.antipyretica,* Columns 4-6: *Callitriche sp.* All taken from a single slow flow area.

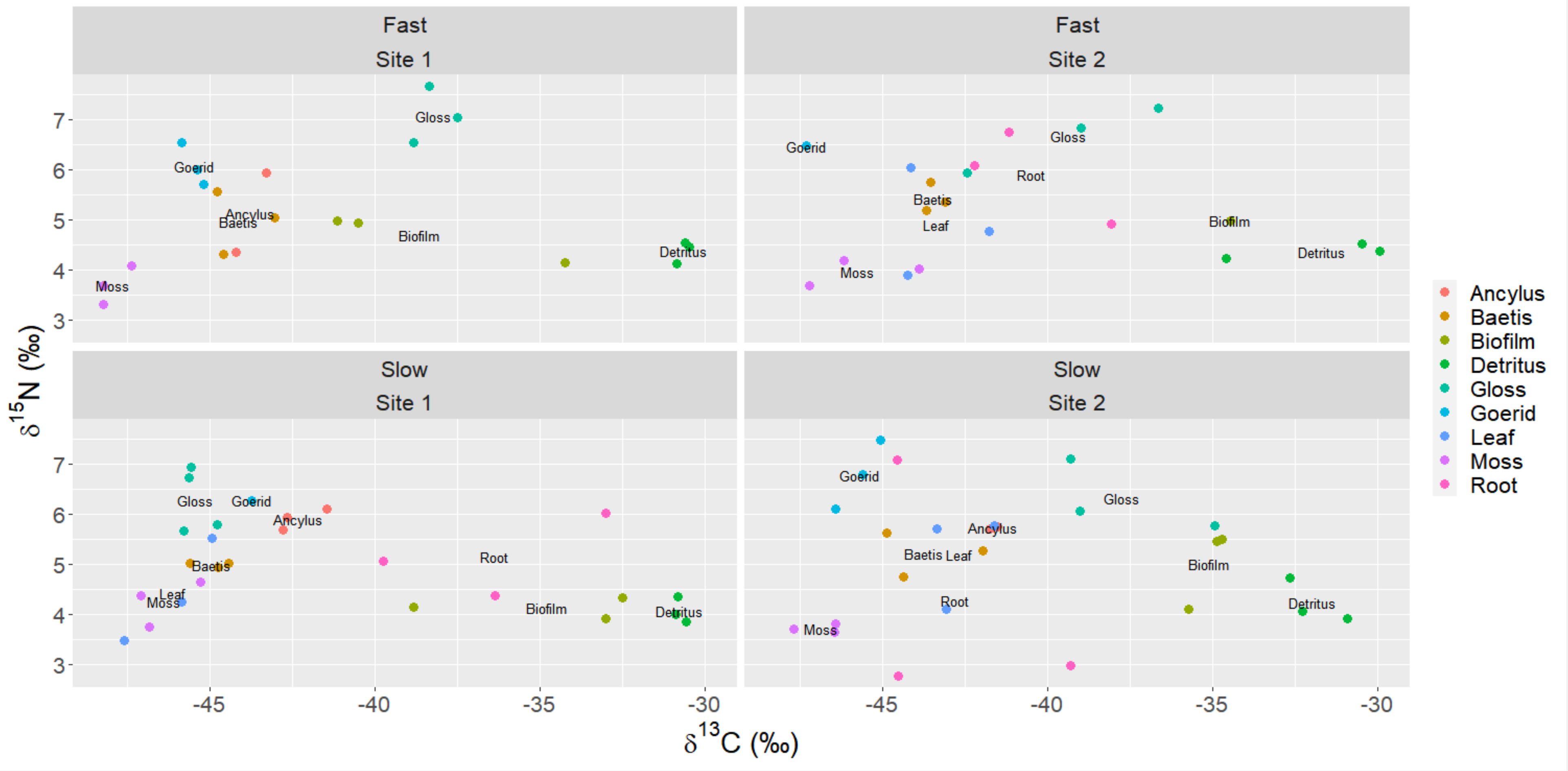


Figure 4 – Stable isotope analysis biplot split by fast and slow sections of a stream**.** Basal and invertebrate samples shown, place of text indicates average position of the named taxon/resource.

The effect of flow regime on $\delta^{13}C$ variability was small when compared to differences between the taxon or resources. When invertebrates and resources were analysed separately:

- Invertebrate taxa site showed a significant influence on the $\delta^{13}C$ values, with upstream sites showing less depletion.
- $\delta^{13}C$ values from basal resources varied with water velocity for all resources apart from moss (*F. antipyrteica*)

1 – Edinburgh Napier 2- UHI

Email: michael.hinchliffe@napier.ac.uk
: @hinchliffe_m